

SEQ ID NO:1

[illegible]

FIG. 1A

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```

3      824  ---CTTCTCTCCCTCTATGGATATAAATTTCAN---CGAACCAGCTATTTAGTGGTCG
4      275  TCACTTCGGCTGCACTA---ACAGACCTTGAACAGGAACCCAGCTATTTAGTGGTCG
2      1
1      251  CACTTTCGCTGCACTA---ACAGACCTTGAACAGGAACCCAGCTGTTTAGTGGTCA
consensus 841  .....

3      879  AAGTGACTTTAGAATCACTACCTTGAATTCGATCCAAAGACCAACATCTTTTATG
4      332  AAGTGACTTTAGAATCACTACCTTGAATTCGATCCAAAGACCAACATCTTTTATG
2      1
1      308  CAGTGACTTCAGTGCACACCTTGAATTCATCCAAAGACCAACATCTTTTATG
consensus 901  .....

3      939  TGGAGGCTTCAGTCTGAAATGAAAGCTTGGGATATAAGGACTGSCAAGGTGATGAGAAG
4      392  TGGAGGCTTCAGTCTGAAATGAAAGCTTGGGATATAAGGACTGSCAAGGTGATGAGAAG
2      11  TGGCGGCTTCAGTCTGAAATCAACGGGCGGATGAGGACTGSCAAGGTGATGAGAAG
1
consensus 961  .....

3      999  CTACAAGGCGACCATCCAGCAGACCTTGGACATCTCTTCCCTCCGGGAAGGCTCCGAGTT
4      452  CTACAAGGCGACCATCCAGCAGACCTTGGACATCTCTTCCCTCCGGGAAGGCTCCGAGTT
2      71  CTACAAGGCGACCATCCAGCAGACCTTGGACATCTCTTCCCTCCGGGAAGGCTCCGAGTT
1
consensus 1021 .....

3      1059 CCTGAGCAGCAGACGCTTCCACCCGGGACTCAGCTGACCGCACCATTATTGCCTGGGA
4      512  CCTGAGCAGCAGACGCTTCCACCCGGGACTCAGCTGACCGCACCATTATTGCCTGGGA
2      131  TCTTAGCAGTACGGACGCTTCCACCCGGGACTCCTGACCGCACCATTATTGCCTGGGA
1
consensus 1081 .....

3      1119 TTTCGGGACCTCTGCCAAATCTCCAACAGATTTTCCACGAGAGGTTCACTGCCCCAG
4      572  TTTCGGGACCTCTGCCAAATCTCCAACAGATTTTCCACGAGAGGTTCACTGCCCCAG
2      191  TTTCGGGACCTCTGCCAAATCTCCAACAGATTTTCCCTTACAGGTTACACTGTGCCAG
1
consensus 1141 .....

3      1179 CCTCGCCTTTCACCCGAGAGAGCCGTGTCTGTCACAGACCAATGGCAACTACCTGGC
4      632  CCTCGCCTTTCACCCGAGAGAGCCGTGTCTGTCACAGACCAATGGCAACTACCTGGC
2      251  CCTCGCCTTTCATCCAAAGGAGCCTGTGTTCCTTGCACAAACCAATGGCAACTACCTGGC
1
consensus 1201 .....

3      1239 CCTTTTCTCCACTGTGTGGCCCTACCGGATGAGCAGACGGCGCGCTATGAAGGGCACAA
4      692  CCTTTTCTCCACTGTGTGGCCCTACCGGATGAGCAGACGGCGCGCTATGAAGGGCACAA
2      311  TCTCTTTTCTCTGTGTGGCCCTATCGGATGAGCAGACGGGATCGCTACCAAGGTCACAA
1
consensus 1261 .....

3      1299 GGTGGAGGGCTACTCAGTGGGCTGCGAGTGTCTCCCGAGCGGTGACTTGTGGTGACGGG
4      752  GGTGGAGGGCTACTCAGTGGGCTGCGAGTGTCTCCCGAGCGGTGACTTGTGGTGACGGG
2      371  GGTGGAGGGCTACTCAGTGGGCTGCGAGTGTCTCCCGAGCGGTGACTTGTGGTGACGGG
1
consensus 1321 .....

3      1359 CAGCGCGGATGGCCGGGTCTGATGTACAGCTTCCGACACAGCCGAGCATGCACACT
4      812  CAGCGCGGATGGCCGGGTCTGATGTACAGCTTCCGACACAGCCGAGCATGCACACT
2      431  CAGCGCTGATGGCCGGGTCTGATGTACAGCTTCCGACACAGCCGAGCATGCACACT
1
consensus 1381 .....

3      1419 GCAGGGGCACACACAGGCTGTGTGGGACCACTATACCCCGTGTGCTTCCGTCTCT
4      872  GCAGGGGCACACACAGGCTGTGTGGGACCACTATACCCCGTGTGCTTCCGTCTCT
2      491  GCAGGGGCACACAGGCTGTGTGGGACCACTATACCCCGTGTGCTTCCGTCTCT
1
consensus 1441 .....

3      1479 CGCCACCTGTCTCTGGGAGGGGACATGAAGATCTGGCACTGAGCTTTTGTCACTCAAC
4      932  CGCCACCTGTCTCTGGGAGGGGACATGAAGATCTGGCACTGAGCTTTTGTCACTCAAC
2      551  CGCCACCTGTCTCTGGGAGGGGACATGAAGATCTGGCACTTTTGTCACTCAAC
1
consensus 1501 .....

```

FIG. 1B

```

3      1539  CTTCCCGATGCCAGCTGGGCTCTTGGACTCCCTCTTCCTCAAGGGTAGATGAGAGGAAC
4      992    CTTCCCGATGCCAGCTGGGCTCTTGGACTCCCTCTTCCTCAAGGGTAGATGAGAGGAAC
2      595    TGCCACTGAGACTG---CCCT---GGG---ATAGG---C
1
consensus 1561 .....

3      1599  GAGCACAGAGGTT--GGCTCTGGGTCCTGGGTACCACTTCTGAGCCTCAGTTTCCTCATC
4      1052  GAGCACAGAGGTT--GGCTCTGGGTCCTGGGTACCACTTCTGAGCCTCAGTTTCCTCATC
2      625  C-GC-CGGAGGTCAAGCTC---TCCGAG---AGCTCTGGGCTTCAGTGA-TCGCG
1
consensus 1621 .....

3      1658  TGTAAAGTGGGA--GAAAAGTCTGTTT--GCCTCAGGAGTGTG--AGGACTACACTAGTGA
4      1111  TGTAAAGTGGGA--GAAAAGTCTGTTT--GCCTCAGGAGTGTG--AGGACTACACTAGTGA
2      675  TATAGCATCGCGGTGAGAAAGCGCTCTCGCGCAAGCCTGTGTCAGAACGGG-TAGCG
1
consensus 1681 .....

3      1714  AAGCGCCTGGCGGGCAGCCGGCGATGCCCAATAAATGTGTGTTTCTGCTTTGTTAAAAA
4      1167  AAGCGCCTGGCGGGCAGCCGGCGATGCCCAATAAATGTGTGTTTCTGCTTTGTTAAAAA
2      734  AAGTCACTGGTGGCGA-----
1
consensus 1741 .....

```

FIG. 1B (continued)

SEQ ID NO:2

GAGGGGTGGACCAAGAGCTTCCGTGTGTGTGTGTGTGTGGAAGTCACCTTTGTGTGACTGTATGGCCTCGCTGGT
GGCATATGATGATTCTGACTCCGAGACCGAGGCTGACCCTGCCAGAAGTGGGGACGCTGCAGGTGTGGAATGCTG
TGGACTCGGGACACTGCCTGCAGACCTACTCTGTGCACAGTGAGGCAGTAAGGGCTGAACGGTGGTCTCCCTGTG
GCCGGCGCATCCTCAGTGGTGGCTTCGACTTTGCCCTGCACCTAACAGACCTTGAAACAGGAACCCAAGTGTTTA
GTGGTCAGAGTGACTTCAGAGTCACCACCTTGAAATTTTCATCCAAAAGAACACAACGTCTTTTtATGTGGCGGCT
TCAGCTCTGAAATCAACAGGNGGGACATGAGGACTGGCAAGGTGGTGAAAGGCTACAAGGCCACCATCCAGCAGA
CCCTGGACATTCTCTTCTCCAGGAGGGCTCCGAGTTTCTTAGCAGTACGGACGCATCCACCCGGGACTCTGCTG
ACCGAACCATTATCGCTGGGATTTCCGGACCGCTGCCAAGATCTCCAACCAGATCTTCCATGAGAGGTACACCT
GTCCCAGCCTCGCCTTGCAATCCAAGGGAGCCTGTGTTCTTGCACAAACCAATGGCAACTACCTGGCTCTCTTTT
CCTCTGTGTGGCCCTATCGGATGAGCAGACGGAGACGCTACGAAGGTCACAAGGTGGAAGGCTACGCGGTGGGCT
GTGAGTGTTCCCCATGTGGTGACCTGCTGGTGACAGGCAGCGCTGATGGCCGGGTTTTGATGTTTCAAGTTTCCGCA
CGGCCAGCCGAGCGTGCGCACTACAAGGGCACACGCAGGCCTGCCTTGGCACCAGCTACCATCCTGTGCTGCCTT
CTGTCTCGGGACCTGCTCCTGGGGAGGAGACATCAAGATCTGGCACTAACTGGCAACTGAGACCTGCCCTGGG
ATAGGCGGCCGGAGGTGAGGCTGCTCCCGAGAGCTGCTGGGCTTCAGTGACTCGGCTATAGCATGGGGGTGAGAA
CGCCGTCTCGGCGCAAGCGTGTGTGAGAACGGGGTAGCCGAAGTGACTGGTGGGCGA

FIG. 2A

SEQ ID NO:3

MMILTPRRLTLPEVGTLLQVWNAVDSGHCLQTYSVHSEAVRAERWSPCGRRLSGGFDFALHLTDLETGTQVFSG
QSDFRVTTLKFHPKEHNVFLCGGFSSEINRXDMRTGKVVKGYKATIQQTLDLFLQEGSEFLSSTDASTRDSADR
TIIAWDFRTAAKISNQIFHERYTCPSLALHPREPVFLLAQTNNGNYLALFSSVWPYRMSRRRRYEGHKVEGYAVGCE
CSPCGDLLVTGSADGRVLMFSFRTASRACALQGHTQACLGTSYHPVLPSVLGTCSWGGDIKIWH

FIG. 2B

Exon 1
SEQ ID NO:4

ATGACAGGCTGGGTGGGCGGCGCCGCCGAGCCTCCCGGTCCCTCGTGGT
ACAGGTGCCCAGAGAACAGACAGCCCGGTTCGAGCTGGATCCTCGGGGC
GCGGCGCCGGGGCGTCAACCGAAGGCCCCGGCGCCACCTCGGCATCCCTC
CCTCGCTCCCGGCGCAGTGACCACCCCTCCTCACTTACCGGCGGCCCC
ACTTCGGCCCCACCAGTCAGCACCCCCAAGTTCAGCCACCGGTACCTCTT
GGGCGTCCGTGGAACACCAGCCGGCTGGAATAACTTCG

Exon 2
SEQ ID NO:5

GAAGTCACCTTTGTGTGACTGTATGGCCTCGCTGGTGGCATATGATGATT
CTGACTCCGAGACCGAGGCTGACCCTGCCAGAAGTGGGGACGCTGCAG

Exon 3
SEQ ID NO:6

CTGCCTGTCTTAAGCCACTAAAACCTGCCTGG
GACGTCCCTCAAACCTTCTCATGATCAAAGCACATTTGAAAGCACAGCTGG
AAATGCCAGCTCTTCTCAGAGGAAAAGGGGTGAGGACTGTGTGCTTCCCT
ATATCCCCAAGAGGCTAAGGCAGCTGCAAGCGCTGAATCCAGAAGCAG

Exon 4
SEQ ID NO:7

TGTCTGAGTTCATCCAGCCATATTTGA
ACAGTCAGTACAGAGAGACTACGGTCCCCAAGAAAGTGCTTTTCCACCTT
CGAGGCCACAGGGGCCCCGTCAACAGCATTCACTGGTGTCCAGTCTTTTG
CAAGAGCCACATGCTTCTCTCTGCTTCCATGGACAAAACCTTCAAG

Exon 5
SEQ ID NO:8

TTCTGCCGTGAACATGGCTATGCA
GGCACCTCTGTGGATCCCGACACAGGCTCCTTTGGGATGGACCCAG

Exon 6
SEQ ID NO:9

GAATCC
CAGAACGAAGGCCTGGCCTGGGCCTTCCTGGCCATGGCTCCCTCAGTCCT
CTGGGCACCACAAAGGCTTTTCCCAGGAAGAGAACGCCTTGCCCTTACT
TGTAAGCTGGGGTTGCCTGGGAG

FIG. 2C

SEQ ID NO:10

ggcacgagggagggagggaggtgagagtgattagtgaggagaagaaaagcaggcccaggaccaagccctggggactg
gggacatcctcggtgacctgtggagcattgagccatgccagctctgtgcctgggtgctgtgctgggttcaagggc
tggtgggagaggtatggaacgccgtggactccgggactgcctgcagacctactccctgcacacagaggcagtg
gggcccgggtgggtccctgtggccggcgcatcctcagtggtggctttgacttcgcgctgcacctaacagacc
ttgaaacaggaacccagctatttagtggtcgaagtgaacttagaatcactaccttgaaattccatccaaaagacc
acaacatctttttatgtggaggcttcagctctgaaatgaaagcttgggatataaggactggcaaggtgatgagaa
gctacaaggcgaccatccagcagaccttggacatcctgttccctccgggaagggtccgagttcctgagcagcacag
acgcttccacccgggactcagctgaccgcaccattattgcctgggatttccggacctctgccaaaatctccaacc
agattttccacgagaggttcacctgccccagcctgccttgacccgagagagcccgtgttccctggcacagacca
atggcaactacctggcccttttctccactgtgtggccctaccggatgagcagacggcgccgctatgaagggcaca
aggtggagggctactcagtggggtgagtgctccccaggcggtgacttgcctgggtgacgggcagcgccgatggcc
gggtcctgatgtacagcttccgcacagccagccgagcatgcacactgcaggggcacacacaggcctgtgtcgga
ccacctaccaccccgctgctgccctccgtcctcgccacctgctcctggggaggggacatgaagatctggcactgag
ctttttgtcactgaaccttcccgatgccagctgggctcctggactccccctcttccctcaagggtagatgagaggaa
cgagcacagaggttggctgtgggtcctgggtaccaccttctgagcctcagtttccctcatctgtaaagtggggaga
aaagtctgtttgcctcaggagtgtgaggactacactagtgaagcgccctggcgggcagccggcgatgcccataa
atgtgtgttttgctgtttgttaaaaaaaaaaaaaaaaaa

FIG. 3A

SEQ ID NO:11

MPALCLVLCWFQGLLGEVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRILSGGFDFALHLTDLETGTQLFSGRS
DFRITTLKFHPKDHNIFLCGGFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTDASTRDSADRTI
IAWDFRTSAKISNQIFHERFTCPSLALHPREPVFLAQTNNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECS
PGDLLVTGSADGRVLMYSFRTASRACTLQHTQACVGTTHPVLPSVLATCSWGDMKIWH

FIG. 3B

M 1 -----GAGGGGTGGACCAAGAGCTTCCGTGT-GTGTTGT-TGTTCGAAGTCAC-----
H 1 GGCACGAGGGAGGGAGCAGGTGAGAGTGATTAGTGGCAGAAGAAAGCAGGCCAGGACC
consensus 1*****.***.*.* * * . * . * . * . * . * . * . * . * . *

M 48 ---CTTTGTGTGACTGT--ATGGCCTCGCTG----GTGG--CATATGATG-ATTCTGAC
H 61 AAGCCCTG-GGGACTGGGACATCCTCGGTGACCCTGTGGAGCAT-TGAGCCATGCCAGC
consensus 61 ...* **.* ***** ..* . ***** ..* . * . * . * . * . * . * . *

M 95 TCCGAGACCGAGGCTGACCTGCCAGAAGTGGGACCTGCAGGTGTGGAATGCTGTGGA
H 119 TCTGTGCTCTGTGCTGTGCTGTGTTCAAGGGCTGTTCGGAGAGGTATGGAACGCCCTGGA
consensus 121 *** * * * . * . * . * * * * * * * * * * * . * . * . * . * . * . *

M 155 CTCGGGCACTGCCTGCAGACCTACTCTGTGCACAGTGAGGCAGTAAGGGCTGAACGGTG
H 179 CTCGGGCACTGCCTGCAGACCTACTCCTGCACACAGAGGCAGTCCGGGCCGCCCGGTG
consensus 181 *** *.*****.*****.*****.*****.*****.*****

M 215 GTCTCCCTGTGGCCGCGCATCCTCAGTGGTGGCTTCGACTTTGCCCTGCACCTAACAGA
H 239 GGCTCCCTGTGGCCGCGCATCCTCAGTGGTGGCTTCGACTTCGCCCTGCACCTAACAGA
consensus 241 * *****.*****.*****.*****.*****.*****.*****

M 275 CCTTGAAACAGGAACCCAAGTGTTTAGTGGTCAGAGTGACTTCAGAGTCACCACCTTGAA
H 299 CCTTGAAACAGGAACCCAGCTATTTAGTGGTCGAAGTGACTTTACAATCACTACCTTGAA
consensus 301 *****.*****.*****.*****.*****.*****.*****

M 335 ATTTCATCCAAAAGAACACAACGTCTTTTTATGTGGCGGCTTCAGCTCTGAAATCAACAG
H 359 ATTTCATCCAAAAGAACACAACATCTTTTTATGTGCAGGCTTCAGCTCTGAAATCAAAGC
consensus 361 *** *****.*****.*****.*****.*****.*****.*****

M 395 GNNGGACATGAGGACTGGCAAGGTGGTGAAGGCTACAAGGCCACCATCCAGCAGACCTT
H 419 TTGGGATATAAGGACTGGCAAGGTGATGAGAAGTACAAGGCCACCATCCAGCAGACCTT
consensus 421 *****.*****.*****.*****.*****.*****.*****

M 455 GGACATCTCTCTCCCTCCAGGAGGGCTCCGAGTTCTTAGCAGTACGGACGCATCCACCCG
H 479 GGACATCTCTCTCCCTCCGGGAAGGCTCCGAGTTCTTAGCAGCACAGACGCTTCCACCCG
consensus 481 ***** ** *****.*****.*****.*****.*****.*****.*****

M 515 GGACTCTGCTGACCGAACCATTATCGCTGGGATTTCCGGACCGCTGCCAAGATCTCCAA
H 539 GGACTCAGCTGACCGCACCATTATCGCTGGGATTTCCGGACCGCTGCCAAGATCTCCAA
consensus 541 ***** *****.*****.*****.*****.*****.*****.*****

M 575 CCAGATCTTCCATGAGAGGTACACCTGTCCCAGCCTCGCCTTGCAATCCAAGGAGCCGT
H 599 CCAGATTTTCCACGAGAGGTACACCTGTCCCAGCCTCGCCTTGCAATCCAAGGAGCCGT
consensus 601 ***** *****.*****.*****.*****.*****.*****.*****

M 635 GTTCCTTGCACAAACCAATGGCAACTACCTGGCTCTCTTTTCCCTGTGTGGCCCTATCG
H 659 GTTCCTTGCACAGACCAATGGCAACTACCTGGCTCTTTTCCCTGTGTGTGGCCCTATCG
consensus 661 ***** *****.*****.*****.*****.*****.*****.*****

M 695 GATGAGCAGACGGAGACGCTACGAAGGTACACAAGGTGGAAGGCTACCGGGTGGGCTGTGA
H 719 GATGAGCAGACGGCGGCGCTATGAAGGACACAAGGTGGAAGGCTACTCAGTGGGCTGCGA
consensus 721 ***** *****.*****.*****.*****.*****.*****.*****

FIG. 4A

```

M      755  GTGTTCCCCATGTCGGTGACCTGCTGGTGACAGGCAGCGCTGATGGCCGGGTTTTGATGTT
H      779  GTGCTCCCCAGGCGGTGACTTGGCTGGTGACGGGCAGCGCCGATGGCCGGGTCCGATGTA
consensus 781  *** ***** * ***** ***** ***** ***** *****

```

```

M      815  CAGTTTCCGCACGGCCAGCCGAGCGTGGCGACTACAAGGGCACACGCAGGCCTGCCCTGG
H      839  CAGCTTCCGCACAGCCAGCCGAGCATGCACACTGCAGGGGCACACAGGCCTGTGTCGG
consensus 841  *** ***** ***** ***** ***** ***** ***** *

```

```

M      875  CACCAGCTACCATCCCTGTGCTGCCCTCTGTCTCTCGGGACCTGCTCCTGGGGAGGAGACAT
H      899  CACCACCTACCAACCGGTGCTGCCCTCCTCTCTCGCCACCTGCTCCTGGGGAGGGGACAT
consensus 901  ***** ***** ** ***** ** ***** ***** *****

```

```

M      935  CAAGATCTGGCACT-----AAC-----TGGCAACTGAGACCTG---
H      959  GAAGATCTGGCACTGAGCTTTTTGTCAGTGAACCTTCCCGATGCCAGCTGGGCTCTTGA
consensus 961  ***** .....** .....** .....*

```

```

M      968  ---CCCT-----GGG-----ATAGG---CG---CC---CGGAGGTGAGGCTGC---TCCC
H      1019 CTCCCTCTTCTCAAGGGTAGATGACAGGAACGAGCACAGAGGT---GGCTGTGGGTCT
consensus 1021 ..*****.....**.....* .....* .....* .....*

```

```

M      1004 CAG---AGCTGCTGGGCTTCAGTGAG-TCCGCTATAGCATGGGGTGAGAACGCCCTCT
H      1078 CGGTACCACCTTCTGAGCCTCAGTTTCCTCATCTGTAA-AGTGGGCAGAAAAGTCTGTT
consensus 1081 *.....* ** ***** ***** ***** ***** *****

```

```

M      1059 CGCCGCAAGCGTGTGTGACAGAACGGG-TAGCCGAAGTCACTGGTGGGCGA-----
H      1137 -GCTCAGGAGTGTG--AGGACTACACTAGTGAAGCGCCTGGCGGGCAGCCGGCGATGC
consensus 1141 . * * * * * ***** .....* .....* .....* .....*

```

```

M
H      1194 CCAATAAATGTGTGTTTGTCTGTTTGTAAAAA
consensus 1201 .....

```

FIG. 4A (continued)


```

M      1  MMILTPRPRIITLPEVGTLOVNNAVDSGHCLQTYSMHSEAVRAERWSPCGRRILSGGFDF
H      1  --MPALCLVLWCWFQLLGEVNNAVDSGHCLQTYSLHTEAVRAARWAPCGRRILSGGFDF
consensus 1  ...      *      *****.*****

```



```

M      61  LHLTDLETGTQVFSGQSDFRMTTLKFHPKEHNVFLCGGSSEINRXDMRTGKVMKGYKAT
H      59  LHLTDLETGTQVFSGRSDFRMTTLKFHPKDHNIFLCGGFSSEMKAWDLRTGKMRSYKAT
consensus 61  *****.*** *****.*****.*****.*****

```



```

M      121 IQOTLDILFLQEGSEFLSSTDASTRDSADRTIIAWDFRTAAKISNQIFHERMTCPSLALH
H      119 IQOTLDILFLREGSEFLSSTDASTRDSADRTIIAWDFRTSAKISNQIFHERETCPSLALH
consensus 121 ***** *****

```



```

M      181 PREPVFLAQTNGNYLALFSSVWPYRMSRRRRYEGHKVEGYAVGCECSPCGDLLVTGSADG
H      179 PREPVFLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPCGDLLVTGSADG
consensus 181 *****.***** *****

```



```

M      241 RVLMEFSFRTASRACALQGHTQACLGTSYHPVLPSVLGTCSWGGDIKIWH
H      239 RVLMSFRTASRACTLQGHTQACVGTITYHPVLPSVLATCSWGGDMKIWH
consensus 241 ****.***** *****.*****.*****.*****

```

FIG. 4B

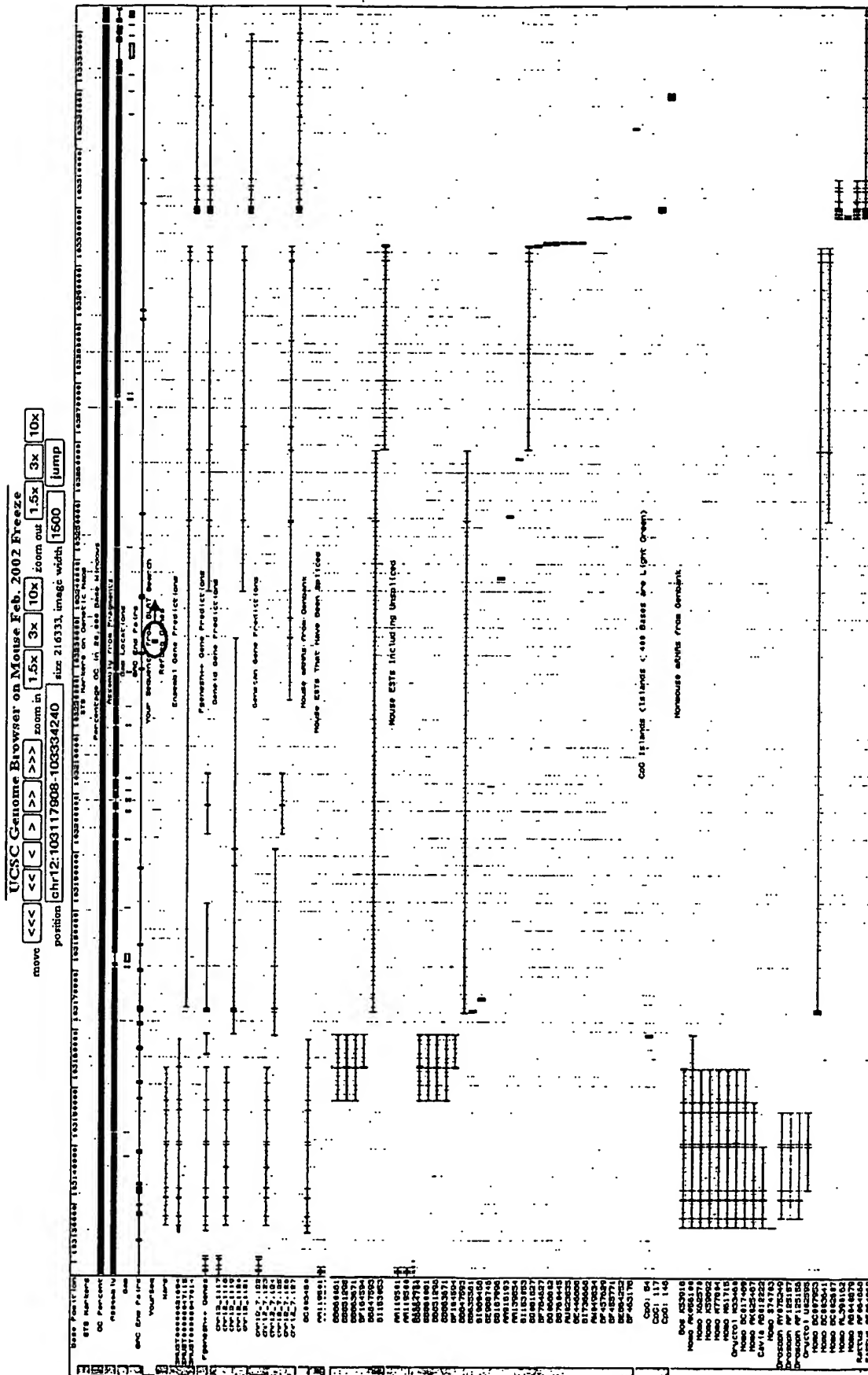


FIG.5A

RapR6

Gene Search vector
Insertion Site

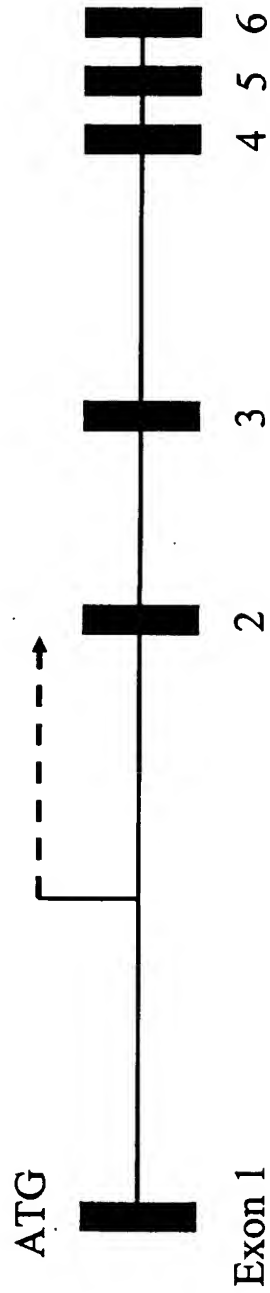


FIG. 5B

chr14:100297347-100312946 size 15600; pixel width 1500 [jump](#)

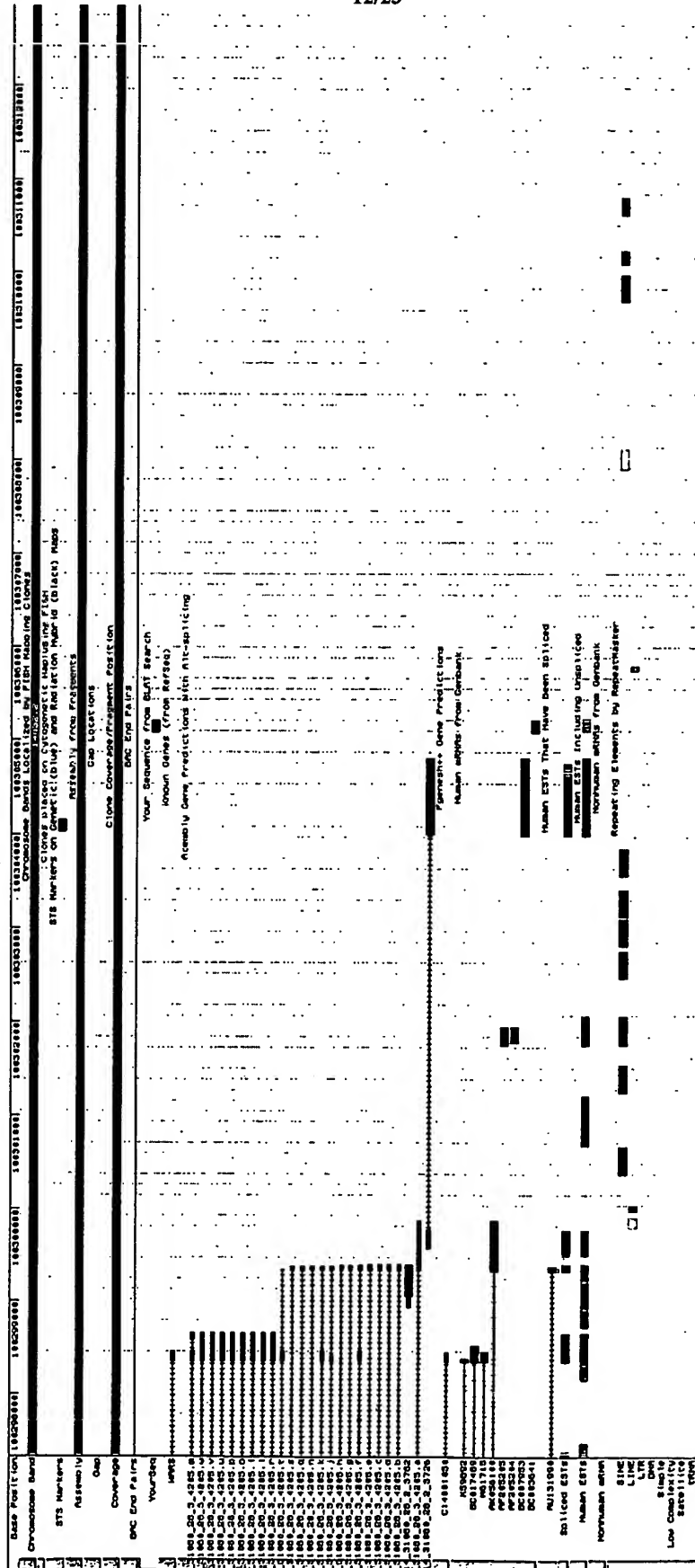


FIG. 6A



Simple
Modular
Architecture
Research
Tool

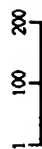
Reference
Kobayashi et al. (1995) Proc. Natl. Acad. Sci. USA 92, 8157-8161
Lemke et al. (2000) Mol. Cell 5, 213-221

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Currently there are too many SMART jobs running.

Your job is no. 1 in the queue.

Your sequence was 100% identical to [sptrmb009BINSLOBTSLK](#), displaying precalculated results.



Mouse over domain / undefined region to see the limits; click on it to go to further annotation; right-click to save whole protein as PNG image
Transmembrane segments as predicted by the [TMHMM2](#) program (TM), coiled coil regions determined by the [Coiled](#) program (C) and Segments of low compositional complexity, determined by the [SEG](#) program (S)

Architecture analysis

Display all proteins with similar domain organization.
Display all proteins with similar domain composition.

The SMART diagram above represents a summary of the results shown below. Domains with scores less significant than established cutoffs are not shown in the diagram. Features are also not shown when two or more occupy the same place of sequence; the priority for display is given by SMART > PFAM > PROSERO repeats > Signal peptide > Transmembrane > Coiled coil > Low complexity. In either case, features not shown in the above diagram are marked 'hidden'.

Confidence predicted domains, repeats, motifs and features:

name	begin	end	E-value
Signal peptide	1	17	-
WD40	24	63	4.30e-05
WD40	66	105	1.40e+00
WD40	108	154	1.90e+02
WD40	203	244	3.30e-01
WD40	247	287	2.90e-03

FIG. 6B

2 possible models considered, only significant TM-segments used

*** the models differ in the number of TM-helices ! ***

-----> STRONGLY preferred model: N-terminus inside
 2 strong transmembrane helices, total score : 1224
 # from to length score orientation
 1 1 21 (21) 510 i-o
 2 210 232 (23) 714 o-i

-----> alternative model
 1 strong transmembrane helices, total score : 812
 # from to length score orientation
 1 6 25 (20) 812 o-i

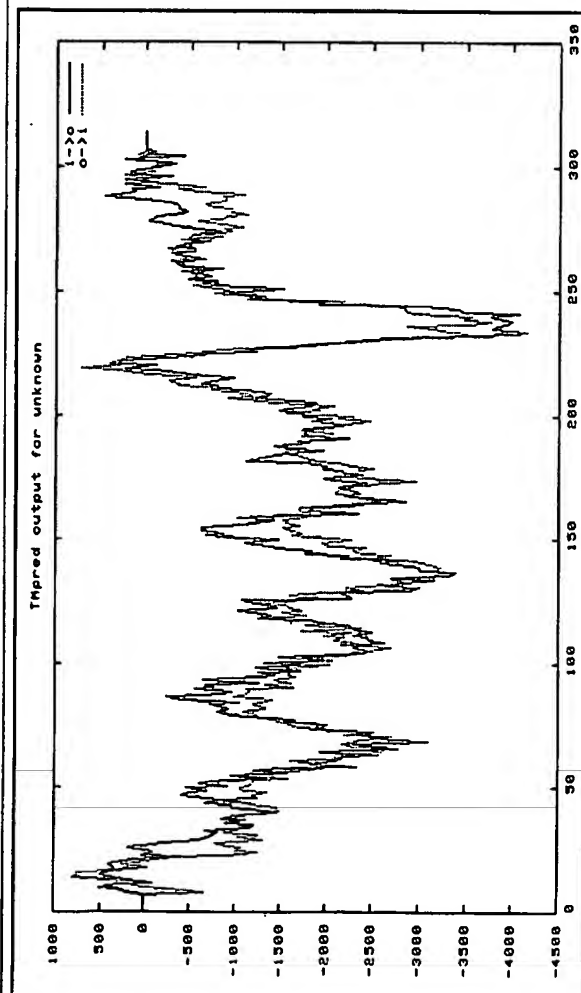


FIG.6C

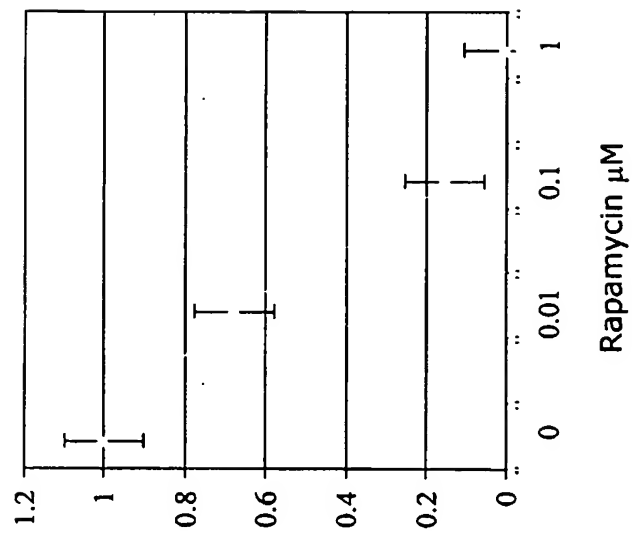


FIG. 7

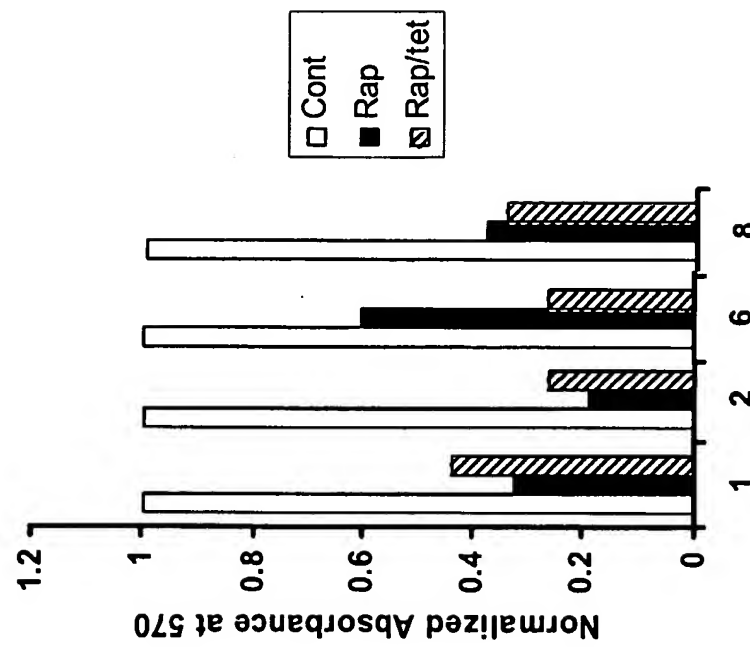


FIG. 8A

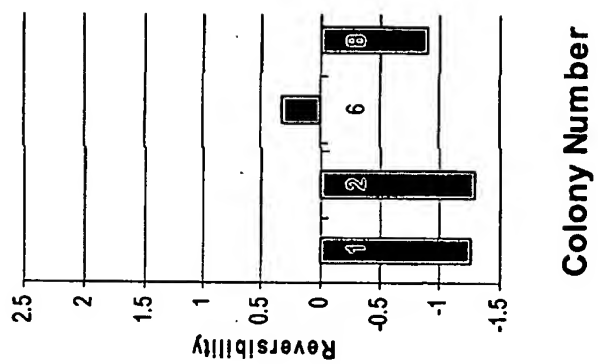


FIG. 8B

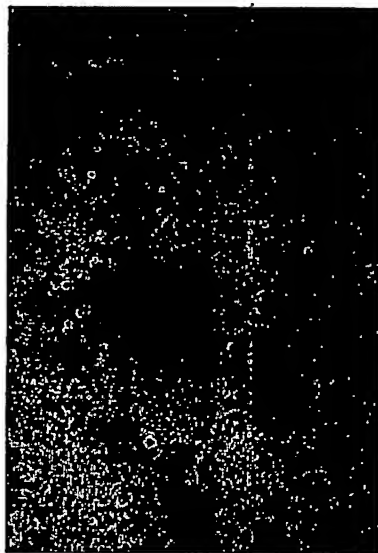


FIG. 8C

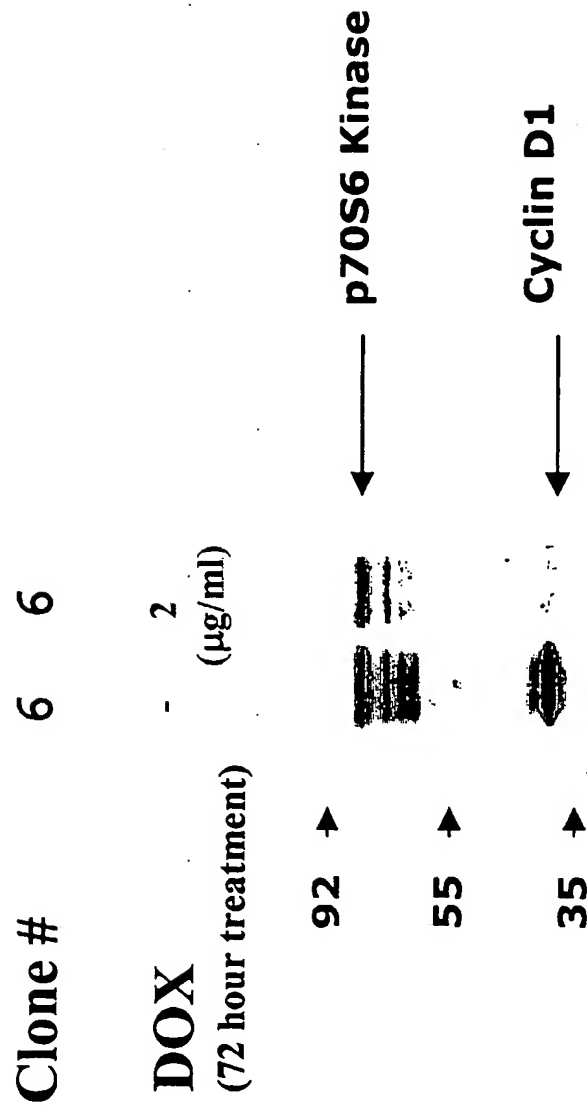


FIG. 8D

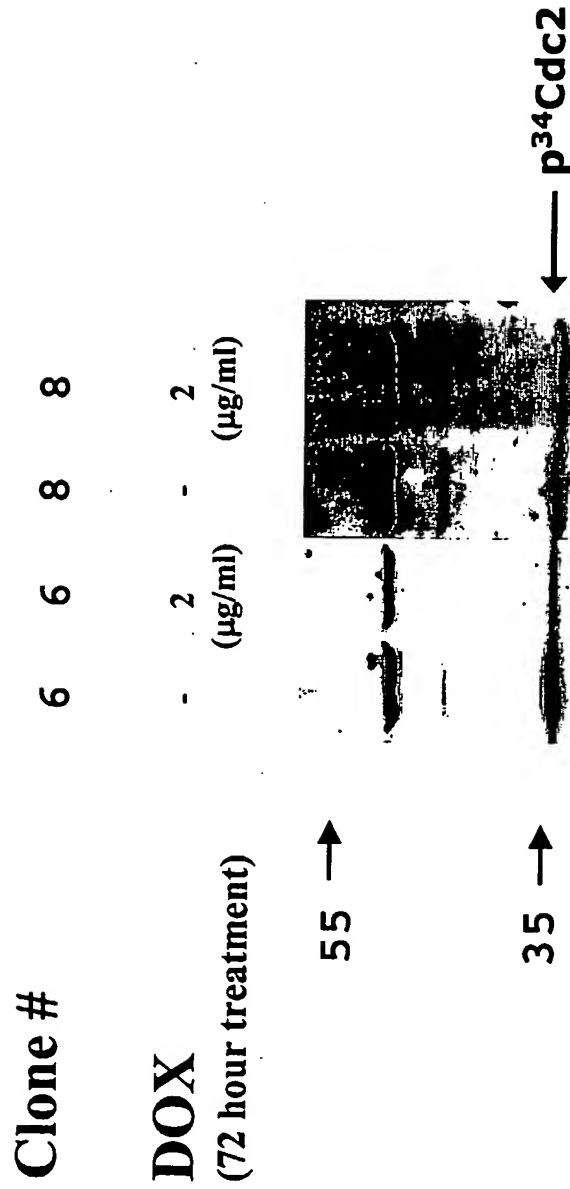


FIG. 8E



FIG. 9A

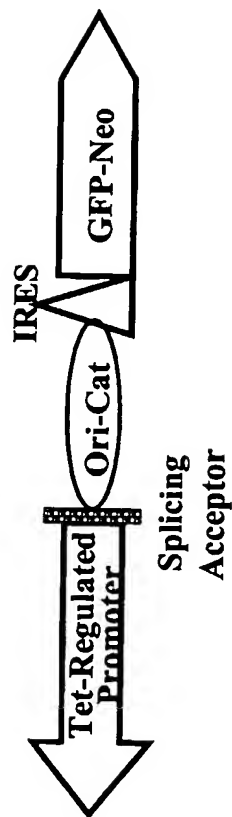


FIG. 9B

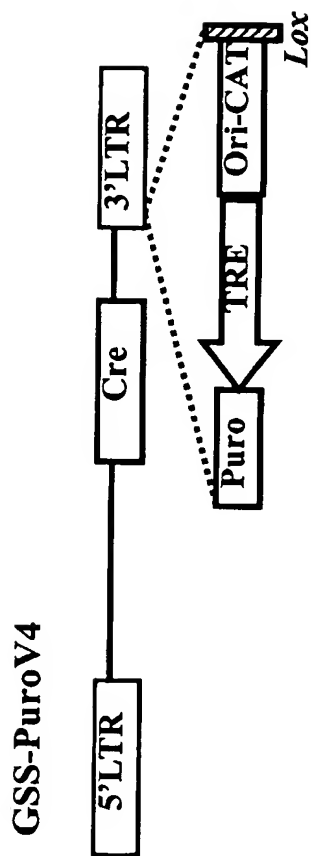


FIG. 9C

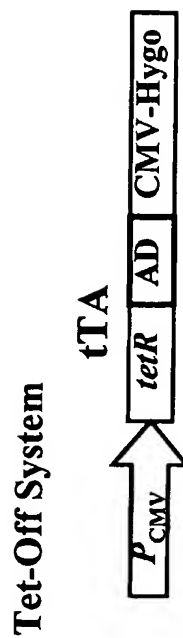


FIG. 9D

10/524433

Accession class	Nucleotide Accession	Nucleotide Position	Filter Orientation	dbSNP rs#	Protein Accession	Function
NCBI RefSeq	<u>NM 024515.1</u>	908	minus strand	<u>rs13065</u>	<u>NP 078791.1</u>	unclassified
		1192	minus strand	<u>rs13492</u>	<u>NP 078791.1</u>	unclassified
GenBank mRNA	<u>BC003641.1</u>	908	minus strand	<u>rs13065</u>	<u>AAH03641.1</u>	unclassified
		1192	minus strand	<u>rs13492</u>	<u>AAH03641.1</u>	unclassified

FIG.10

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